

ABSTRACT OF THE DISCLOSURE

A method of identifying putative naturally occurring antisense transcripts is provided. The method is effected by (a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and (b) identifying expressed polynucleotide sequences from the second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of the first database, thereby identifying putative naturally occurring antisense transcripts. Also provided are polynucleotides and polypeptide sequences identified by the above-described methodology.